

OIPE

## RAW SEQUENCE LISTING

DATE: 10/29/2001

PATENT APPLICATION: US/09/910,059

TIME: 15:18:02

Input Set : A:\pto\_vsk.txt

Output Set: N:\CRF3\10292001\I910059.raw

3 <110> APPLICANT: Copley, Clive G  
 4 Edge, Michael Derek  
 5 Emery, Stephen Charles  
 7 <120> TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said  
 Antibody, and  
 8 Their Therapeutic use in an Adept System  
 10 <130> FILE REFERENCE: 1991-209  
 12 <140> CURRENT APPLICATION NUMBER: US 09/910,059  
 13 <141> CURRENT FILING DATE: 2001-07-23  
 15 <150> PRIOR APPLICATION NUMBER: US 09/171,945  
 16 <151> PRIOR FILING DATE: 1998-10-29  
 18 <150> PRIOR APPLICATION NUMBER: PCT/GB97/01165  
 19 <151> PRIOR FILING DATE: 1997-04-29  
 21 <150> PRIOR APPLICATION NUMBER: GB 9703103.3  
 22 <151> PRIOR FILING DATE: 1997-02-14  
 24 <150> PRIOR APPLICATION NUMBER: GB9609405.7  
 25 <151> PRIOR FILING DATE: 1996-05-04  
 27 <160> NUMBER OF SEQ ID NOS: 131  
 29 <170> SOFTWARE: PatentIn version 3.1  
 31 <210> SEQ ID NO: 1  
 32 <211> LENGTH: 32  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Artificial Sequence  
 36 <220> FEATURE:  
 37 <223> OTHER INFORMATION: light chain cDNA foward primer  
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 44 <211> LENGTH: 31  
 45 <212> TYPE: DNA  
 46 <213> ORGANISM: Artificial Sequence  
 48 <220> FEATURE:  
 49 <223> OTHER INFORMATION: heavy chain cDNA foward primer  
 51 <400> SEQUENCE: 2  
 52 ggaagcttag acagatgggg gtgtcgtttt g 31  
 55 <210> SEQ ID NO: 3  
 56 <211> LENGTH: 34  
 57 <212> TYPE: PRT  
 58 <213> ORGANISM: Mus musculus  
 60 <400> SEQUENCE: 3  
 62 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala  
 63 1 5 10 15  
 66 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
 67 20 25 30  
 70 Tyr Met  
 74 <210> SEQ ID NO: 4  
 75 <211> LENGTH: 24  
 76 <212> TYPE: DNA

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77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: light chain cDNA backward primer ✓
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89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
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94 <400> SEQUENCE: 5
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101 <213> ORGANISM: Artificial Sequence ✓
103 <220> FEATURE:
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106 <400> SEQUENCE: 6
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112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence ✓
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122 <210> SEQ ID NO: 8
123 <211> LENGTH: 357
124 <212> TYPE: DNA
125 <213> ORGANISM: Mus musculus
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130 ataacctgca gtgccagctc aagtgttaact tacatgcact gggtccagca gaagccaggc 120
132 acttctccca aactctggat ttatagcaca tccaacctgg cttctggagt ccctgctcgc 180
134 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
136 gatgctgcca cttattactg ccagcaaaagg agtacttacc cgctcacgtt cggtgctggg 300
138 accaagctgg agctgaaaacg ggctgatgct gcaccaactg tatccatctt caagctt 357
141 <210> SEQ ID NO: 9
142 <211> LENGTH: 108
143 <212> TYPE: PRT
144 <213> ORGANISM: Mus musculus
146 <400> SEQUENCE: 9
148 Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
149 1 5 10 15
152 Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
153 20 25 30

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156 His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
157      35      40      45
160 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
161      50      55      60
164 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
165 65      70      75      80
168 Asp Ala Ala Thr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
169      85      90      95
172 Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala
173      100      105
176 <210> SEQ ID NO: 10
177 <211> LENGTH: 360
178 <212> TYPE: DNA
179 <213> ORGANISM: Mus musculus
181 <400> SEQUENCE: 10
182 gaggtgcagc tgcagcartc wggggcagag cttgtgaggt caggggcctc agtcaagttg      60
184 tcctgcacag cttctggctt caacattaaa gacaactata tgcactgggt gaagcagagg      120
186 cctgaacagg gcctggagtg gattgcatgg attgatoctg agaatgggtga tactgaatat      180
188 gccccgaagt tccggggcaa ggccactttg actgcagact catcctccaa cacagcctac      240
190 ctgcacctca gcagcctgac atctgaggac actgccgtct attactgtca tgtcctgatc      300
192 tatgctgggtt atttggctat ggactactgg ggtcaaggaa cctcagtcgc cgtctcctca      360
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196 <211> LENGTH: 120
197 <212> TYPE: PRT
198 <213> ORGANISM: Mus musculus
200 <400> SEQUENCE: 11
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203 1      5      10      15
206 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
207      20      25      30
210 Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
211      35      40      45
214 Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
215      50      55      60
218 Arg Gly Lys Ala Thr Leu Thr Ala Asp Ser Ser Ser Asn Thr Ala Tyr
219 65      70      75      80
222 Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
223      85      90      95
226 His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
227      100      105      110
230 Gly Thr Ser Val Ala Val Ser Ser
231      115      120
234 <210> SEQ ID NO: 12
235 <211> LENGTH: 39
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: light chain primer
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243 aagctttccc gcggggacat tgagctcacc cagtctcca      39
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248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: light chain primer ✓
254 <400> SEQUENCE: 13
255 aagcttctcg agcttgggtcc cagcaccgaa      30
258 <210> SEQ ID NO: 14
259 <211> LENGTH: 36
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence ✓
263 <220> FEATURE:
264 <223> OTHER INFORMATION: heavy chain primer ✓
266 <400> SEQUENCE: 14
267 aagcttggaa ttcagtgtga ggtgcagctg cagcag      36
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272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence ✓
275 <220> FEATURE:
276 <223> OTHER INFORMATION: heavy chain primer ✓
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279 aagcttcgag ctcacggcga ctgaggttcc ttg      33
282 <210> SEQ ID NO: 16
283 <211> LENGTH: 705
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence ✓
287 <220> FEATURE:
288 <223> OTHER INFORMATION: chimaeric light chain sequence ✓
290 <400> SEQUENCE: 16
291 atggattttc aagtgcagat tttcagcttc ctgctaataca gtgcttcagt cataatgtcc      60
293 cgcgggggaca ttgagctcac ccagtctcca gcaatcatgt ctgcatctcc agggggagaag      120
295 gtcaccataa cctgcagtgc cagctcaagt gtaacttaca tgcaactggtt ccagcagaag      180
297 ccaggcactt ctcccaaact ctggatttat agcacatcca acctggcttc tggagtccct      240
299 gctcgcttca gtggcagtgg atctgggacc tcttactctc tcacaatcag ccgaatggag      300
301 gctgaagatg ctgccactta ttactgccag caaaggagta cttaccgcgt cacgttcggt      360
303 gctgggacca agctcgagat caaacggact gtggctgcac catctgtctt catcttcccg      420
305 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      480
307 tatcccagag aggccaaaagt acagtggaag gtggataacg ccctccaatc gggtaaactcc      540
309 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacccctg      600
311 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag      660
313 ggcttgagtt cgcccgtcac aaagagcttc aacaggggag agtgt      705
316 <210> SEQ ID NO: 17
317 <211> LENGTH: 235
318 <212> TYPE: PRT
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:

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322 &lt;223&gt; OTHER INFORMATION: chimaeric light chain sequence

324 &lt;400&gt; SEQUENCE: 17

326 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser

327 1 5 10 15

330 Val Ile Met Ser Arg Gly Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile

331 20 25 30

334 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser

335 35 40 45

338 Ser Ser Val Thr Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser

339 50 55 60

342 Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro

343 65 70 75 80

346 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile

347 85 90 95

350 Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg

351 100 105 110

354 Ser Thr Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys

355 115 120 125

358 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

359 130 135 140

362 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

363 145 150 155 160

366 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln

367 165 170 175

370 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser

371 180 185 190

374 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

375 195 200 205

378 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser

379 210 215 220

382 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

383 225 230 235

386 &lt;210&gt; SEQ ID NO: 18

387 &lt;211&gt; LENGTH: 765

388 &lt;212&gt; TYPE: DNA

389 &lt;213&gt; ORGANISM: Artificial Sequence

391 &lt;220&gt; FEATURE:

392 &lt;223&gt; OTHER INFORMATION: chimaeric HuIgG2 Fd construct

394 &lt;400&gt; SEQUENCE: 18

395 atgaagtgt ggctgaactg gattttcctt gtaacacttt taaatggaat tcagtgtgag 60

397 gtgcagctgc agcartcagg ggcagagctt gtgaggctcag gggcctcagt caagttgtcc 120

399 tgcacagctt ctggcttcaa cattaaagac aactatatgc actgggtgaa gcagaggcct 180

401 gaacagggcc tggagtggat tgcattgatt gatcctgaga atggtgatac tgaatatgcc 240

403 ccgaagtcc ggggcaaggc cactttgact gcagactcat cctccaacac agcctacctg 300

405 cacctcagca gcctgacatc tgaggacact gccgtctatt actgtcatgt cctgatctat 360

407 gctggttatt tggctatgga ctactggggt caaggaacct cagtcgccgt gagctcggct 420

409 agcaccaagg gaccatcggt ctccccctg gccccctgct ccaggagcac ctccgagagc 480

411 acagccgccc tgggtgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 540

413 aactcaggcg ctctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 600

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/910,059

DATE: 10/29/2001

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